RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/441,966B_

Source: _1FW16_

Date Processed by STIC: _11/23/04_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 11/23/2004
PATENT APPLICATION: US/09/441,966B   TIME: 14:45:41

Input Set : A:\AERO1120-1.txt
Output Set: N:\CRF4\11222004\I441966B.raw

```
 3 <110> APPLICANT: AEROVANCE, INC.
 4        Hall, Roderick L.
 5        Poll, Christopher T.
 6        Newton, Benjamin B.
 7        Taylor, William J.A.
 9 <120> TITLE OF INVENTION: Method For Accelerating The Rate Of Mucociliary Clearance
11 <130> FILE REFERENCE: AERO1120-1
13 <140> CURRENT APPLICATION NUMBER: US 09/441,966B
14 <141> CURRENT FILING DATE: 1999-11-17
16 <150> PRIOR APPLICATION NUMBER: US 09/218,913
17 <151> PRIOR FILING DATE: 1998-12-22
19 <160> NUMBER OF SEQ ID NOS: 106
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 179
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1
30 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
31 1               5                   10                  15
34 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
35             20                  25                  30
38 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
39          35                  40                  45
42 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
43       50                  55                  60
46 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
47 65                  70                  75                  80
50 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
51                  85                  90                  95
54 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
55              100                 105                 110
58 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
59          115                 120                 125
62 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
63       130                 135                 140
66 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
67 145                 150                 155                 160
70 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
71                  165                 170                 175
74 Ala Val Ser
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 197
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 80 <212> TYPE: PRT
 81 <213> ORGANISM: Homo sapiens
 83 <220> FEATURE:
 84 <221> NAME/KEY: SIGNAL
 85 <222> LOCATION: (1)..(18)
 86 <223> OTHER INFORMATION:
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 91 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
 92 1               5                  10                  15
 95 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
 96               20                  25                  30
 99 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
100               35                  40                  45
103 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
104       50                  55                  60
107 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
108 65                  70                  75                  80
111 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
112                   85                  90                  95
115 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
116               100                 105                 110
119 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
120               115                 120                 125
123 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
124       130                 135                 140
127 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
128 145                 150                 155                 160
131 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
132                   165                 170                 175
135 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
136               180                 185                 190
139 Ala Gly Ala Val Ser
140             195
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 153
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
148 <400> SEQUENCE: 3
150 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
151 1               5                  10                  15
154 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
155               20                  25                  30
158 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
159             35                  40                  45
162 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
163       50                  55                  60
166 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
167 65                  70                  75                  80
170 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
```

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171                 85              90                  95
174 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
175             100             105             110
178 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
179         115             120             125
182 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
183     130             135             140
186 Ala Cys Met Leu Arg Cys Phe Arg Gln
187 145             150
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 58
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 4
197 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
198 1               5               10              15
201 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
202             20              25              30
205 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
206         35              40              45
209 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
210     50              55
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 51
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 5
220 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
221 1               5               10              15
224 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
225             20              25              30
228 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
229         35              40              45
232 Lys Lys Cys
233     50
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 58
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
243 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
244 1               5               10              15
247 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
248             20              25              30
251 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
252         35              40              45
255 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
256     50              55
259 <210> SEQ ID NO: 7
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Input Set : A:\AERO1120-1.txt
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260 <211> LENGTH: 51
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 7
266 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
267 1               5                   10                  15
270 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
271             20                  25                  30
274 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
275         35                  40                  45
278 Leu Arg Cys
279     50
282 <210> SEQ ID NO: 8
283 <211> LENGTH: 92
284 <212> TYPE: PRT
285 <213> ORGANISM: Homo sapiens
287 <400> SEQUENCE: 8
289 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
290 1               5                   10                  15
293 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
294             20                  25                  30
297 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
298         35                  40                  45
301 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
302     50                  55                  60
305 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
306 65                  70                  75                  80
309 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
310             85                  90
313 <210> SEQ ID NO: 9
314 <211> LENGTH: 708
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Consensus DNA sequence of human Bikunin (Fig. 3).
321 <220> FEATURE:
322 <221> NAME/KEY: misc_feature
323 <222> LOCATION: (622)..(622)
324 <223> OTHER INFORMATION: "n" is any nucleotide.
327 <220> FEATURE:
328 <221> NAME/KEY: misc_feature
329 <222> LOCATION: (679)..(679)
330 <223> OTHER INFORMATION: "n" is any nucleotide.
333 <220> FEATURE:
334 <221> NAME/KEY: misc_feature
335 <222> LOCATION: (707)..(707)
336 <223> OTHER INFORMATION: "n" is any nucleotide.
339 <400> SEQUENCE: 9
340 ggccgggtcg tttctcgcct ggctgggatc gctgctcctc tctggggtcc tggcggccga      60
```

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    342 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc   120
    344 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg   180
    346 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc   240
    348 cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc   300
    350 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta   360
    352 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcatcct tcccacgctg   420
    354 gtactttgac gtggagagga actcctgcaa taacttcatc tatggaggct gccggggcaa   480
    356 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa   540
    358 tcctcccctg cccctttggct caaaggtggt ggttctggcc ggggctgttt cgtgatggtg   600
W--> 360 ttgatccttt tcctggggag cntccatggt cttactgatt ccgggtggca aggaggaacc   660
    362 aggagcgtgc cctgcgganc gtctggagct tcggagatga caagggnt               708
    365 <210> SEQ ID NO: 10
    366 <211> LENGTH: 197
    367 <212> TYPE: PRT
    368 <213> ORGANISM: Artificial Sequence
    370 <220> FEATURE:
    371 <223> OTHER INFORMATION: Amino acids -18 to 179 of the translation of the consensus
DNA
    372         sequence in Fig. 3.
    374 <400> SEQUENCE: 10
    376 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
    377 1               5                  10                  15
    380 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
    381             20                  25                  30
    384 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
    385             35                  40                  45
    388 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
    389         50                  55                  60
    392 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
    393 65                  70                  75                  80
    396 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
    397             85                  90                  95
    400 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
    401             100                 105                 110
    404 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
    405         115                 120                 125
    408 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
    409     130                 135                 140
    412 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
    413 145                 150                 155                 160
    416 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
    417             165                 170                 175
    420 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
    421             180                 185                 190
    424 Ala Gly Ala Val Ser
    425         195
    428 <210> SEQ ID NO: 11
    429 <211> LENGTH: 179
    430 <212> TYPE: PRT
    431 <213> ORGANISM: Artificial Sequence
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 622,679,707
Seq#:11; Xaa Pos. 8,17,19,21,22,23,24,25,26,40,42,45,46,47,52,64,103,112
Seq#:11; Xaa Pos. 114,116,117,118,119,120,121,135,137,140,141,142,147,159
Seq#:12; N Pos. 361,367,384,390
Seq#:14; N Pos. 424,481,509
Seq#:16; N Pos. 3,11,12,17,48,425
Seq#:17; N Pos. 6,401,407
Seq#:48; N Pos. 1358
Seq#:51; N Pos. 46,117,313
Seq#:72; Xaa Pos. 9,11,17,19
Seq#:74; Xaa Pos. 25
Seq#:75; N Pos. 425,482,510
Seq#:76; Xaa Pos. 25
Seq#:77; N Pos. 45,49,118,231,305
Seq#:78; N Pos. 117,123,321
Seq#:79; N Pos. 9,11,222,231,262,267,274
Seq#:80; N Pos. 44,46,76,114,187,268,309,317,332,370
Seq#:81; N Pos. 35,148,235,261,272,293,300,313,320
Seq#:82; N Pos. 56,137,145,159,233
Seq#:83; N Pos. 20,26,95,292,313,314,315
Seq#:84; N Pos. 27,139,223,232,302,310,322,328,357,375,392,398,405,427,437
Seq#:84; N Pos. 449,458,474
Seq#:85; N Pos. 361,367,384,390
Seq#:86; N Pos. 3,11,12,17,48,425
Seq#:87; N Pos. 7,403,409
Seq#:88; N Pos. 48,62,211,232,245,309,318
Seq#:89; N Pos. 424,481,509
Seq#:90; N Pos. 257
Seq#:91; N Pos. 19,147
Seq#:92; N Pos. 33,55,213,228,259,267,324,333,344,387
Seq#:93; N Pos. 306,328,342,365,370,377,382,402
Seq#:94; N Pos. 1,142,339,347
Seq#:95; N Pos. 334,368,376
Seq#:96; N Pos. 108,261
Seq#:97; N Pos. 20,30
Seq#:98; N Pos. 45,102,105,159,174,213,337
Seq#:100; N Pos. 304,309
Seq#:101; N Pos. 24
Seq#:102; N Pos. 61,74,122,184
Seq#:103; N Pos. 7
Seq#:104; N Pos. 32,67,136
Seq#:105; N Pos. 13,19,107

<pre>
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L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:86
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:600
M:341 Repeated in SeqNo=9
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:360
L:704 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:701
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:420
M:341 Repeated in SeqNo=14
L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1410 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:45,Line#:1407
L:1522 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:47,Line#:1519
L:1640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:1320
L:1660 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:49,Line#:1657
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
M:341 Repeated in SeqNo=51
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
M:341 Repeated in SeqNo=72
L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:16
L:2423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:420
M:341 Repeated in SeqNo=75
L:2449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:16
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0
M:341 Repeated in SeqNo=77
L:2528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:60
M:341 Repeated in SeqNo=78
L:2587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
M:341 Repeated in SeqNo=79
L:2664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
M:341 Repeated in SeqNo=80
L:2741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
M:341 Repeated in SeqNo=81
L:2790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:2837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83
L:2966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:3025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:360
L:3064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
M:341 Repeated in SeqNo=86
L:3105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
M:341 Repeated in SeqNo=87
L:3170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88 after pos.:0
M:341 Repeated in SeqNo=88
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Input Set : A:\AERO1120-1.txt
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L:3221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:420
M:341 Repeated in SeqNo=89
L:3246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:240
L:3267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
M:341 Repeated in SeqNo=91
L:3350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92 after pos.:0
M:341 Repeated in SeqNo=92